App No.: 10/087,190 Docket No.: 511582003420 Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN
ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 1 of 36

#### Figure 1: 121P1F1 SSH sequence of 254 nucleotides (SEQ ID:1)

1 GATCACAGTC TTTGTATTTT TCTACTTCTG CCTTTAGCTG TTCCCTTTGG TCTCGAAGTG

61 AAGAAAGCTC TTTTGCTAGC CTGGTTCGCT CTTCCGTTTC ACATCGGCCA ATTTTAGCTT

121 TCTCAATGCT TTTCTGTAGG CTTGCATGCT TTTGACTTCC CTCAGACAAC TGAGATTCCA

181 GAACCTCCAA CTTATGTTTC CTTGCATGAA GAGCTTTACT TGGAAAAGCC CAATAATAAT

241 TAGAAGTTCC GATC

#### Figure 2: The cDNA and Amino Acid Sequence(s)

Figure 2A. The cDNA (SEQ ID. NO:2) and amino acid sequence (SEQ ID. NO:3) of 121P1F1. The start methionine is underlined. The open reading frame extends from nucleic acid 82-699 including the stop codon.

1 ccaaaatcaaacgcgtccgggcctgtcccgccctctccccaagcgcqgqcccggccagc MSKKKGLSAEEK 61 ggaagcccttgcgcccqcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA RMMEIFSETKDVFQLKDL 121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG 34 K I A P K E K G I T A M S V K E V L 181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC DDGMVDCERI G T S 241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT 74 F P S K A L H A R K H K L E V L E S 301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG 94 S E G S Q K H A S L Q K S I E K A K I G 361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC E. R T R L A K E L S S L R D Q 421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAA 134 R E Q L K A E V E K Y·K D C D P Q V V E 481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA 154 E I R Q A N K V A K E A A N R W Т 541 GAAATACGCCAAGCAAATAAAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATA 174 F A I K S W A K R K F G F E E N K 601 TTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGA GIPEDFDYID 661 ACTTTTGGAATTCCAGAAGACTTTGACTACATAGACTAAAatattccatggtggtgaagg 841 aaaaaaaaaaaaaaaaaaaaaa

App No.: 10/087,190 Inventor: Pia M. CHALLITA-EID et al. Docket No.: 511582003420

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.

REPLACEMENT SHEET

Sheet 2 of 36

Figure 2B. The cDNA (SEQ ID. NO:4) and amino acid sequence (SEQ ID. NO:5) of 121P1F1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

		1	cc	aaa	atc	aaa	cgc	gtc	cgg	gaat	tgt	ccc	gcc	ecto	ctc	ccc	aag	cgc	ggg	cccggccagc
1								M	S	K	K	K	G	L	S	А	E	E	K	R
61	gg	aag	ccc	ctg	cgc	ccg	cgc	cAT	GTC	AAA)	GAA	AAA	AGG	ACTO	GAG	rgc	AGA?	AGA	AAA	GAGA
14	Т	R	М	M	Ε	I	F	S	E	T	K	D	V	F	Q	L	K	D	L	E
121	AC	TCG	САТ	GAT	GGA	AAT.	ATT'	TTC'	rga <i>i</i>	AAC	\AA/	AGA:	rgtz	TTF	rca/	TTA	AAA	AGA	CTT	GGAG
34	K	I	Α	Р	K	E	K	G	I	T	A	М	S	V	K	E	V	L	Q	S
181	AA	GAT	TGC	TCC	CAA	AGA	GAA	AGG	CAT	rac:	rgc:	rato	STC	AGTA	AAA	AGA/	AGT	CCT'	rca.	AAGC
54	L	V	D	D	G	M	V	D	С	E	R	I	G	Т	S	N	Y	Y	W	А
241	тт	AGT	TGA	TGA	TGG	TAT	GGT'	rga(	CTG	ГGА	GAG	GATO	CGGZ	AAC	rTC:	raa:	TA?	TTA	rtg	GGCT
74	F	Р	S	K	A	L	Н	A	R	K	Н	K	L	E	V	L	E	S	Q	D
301	TT	TCC.	AAG	TAA	AGC	TCT	TCA'	rgc <i>i</i>	AAG	GAAA	ACA:	raac	STTO	GGA	GT:	CTC	GGA/	ATC	rca(	GGAC
94	Р	G	С	С	F	Н	E	I	I	K	V	Ş	Y	Y	R	K	F	M	L	G
361	CC	TGG	CTG	CTG	CTT	CCA'	rga.	TAP	TAP	raa <i>i</i>	AGTO	CTC	CTA	TAT	rag <i>i</i>	\AA/	TTA	CTG	GCT	GGC
114	A	V	Α	Н	A	С	N	P	S	Т	L	G	G	*						
421	GC.	AGT	GGC'	TCA	CGC	CTG'	raa'	rcc	CAG	CACT	ГТТС	GGG <i>I</i>	AGG(	CTGA	Aggo	cgg	gcaq	gato	cac	gagg
481	tg	act	ttc	ccc	cac	ccc	caca	atga	aagt	gca	aaga	atg	gagt	tgt	ctq	gago	ggaa	agto	caaa	aagc
541	at	gca	agc	cta	cag	aaa	agca	atto	gaga	aaaq	gcta	aaaa	att	ggc	cgat	gt	gaaa	acg	gaaq	gagc
601	ga	acc.	agg	cta	gca	aaa	gag	cttt	ctt	cac	ctto	cgaç	gaco	caaa	agg	gaad	cago	ctaa	aag	gcag
661	aa	gta	gaa	aaa	tac	aaa	gact	gt	gato	ccgc	caaç	gtto	gtg	gaaç	gaaa	atad	ege	caaq	gcaa	aata
721	aa	gta	gcc	aaa	gaa	gct	gcta	aaca	agat	gga	acto	gata	aca	atat	tc	gcaa	itaa	aaat	ctt	ggg
781	CC	aaa	aga	aaa	ttt	ggg	ttt	gaaq	gaaa	aata	aaaa	atto	gata	agaa	actt	ttç	ggaa	atto	cca	gaag
841	ac	ttt	gac	tac	ata	gac	taaa	aata	atto	ccat	ggt	ggt	gaa	agga	atgt	aca	aago	ette	gtga	aata
901	tg	taa	att	tta	aac	tat	tato	ctaa	acta	aagt	gta	acto	gaat	tgt	cgt	ttç	gaat	gta	aact	gtg
961	tt	tat	cat	ttt	att	aato	gtta	aaat	caaa	agto	gtaa	aaat	gca	aaaa	aaa	aaa	aaaa	aaaa	aaaa	aaa
1021	aa	aaa	aaa																	

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 3 of 36

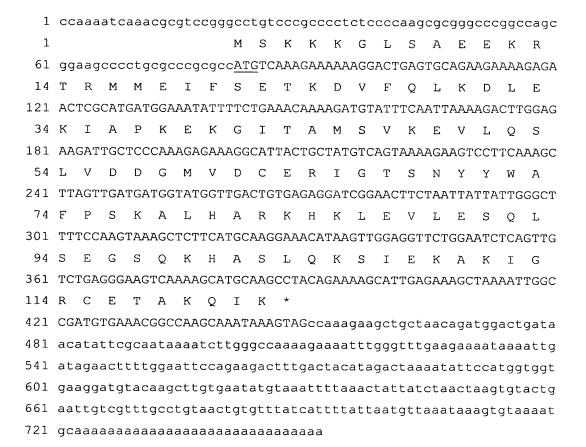
Figure 2C. The cDNA (SEQ ID. NO:6) and amino acid sequence (SEQ ID.NO:7) of 121P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

1 ccaaaatcaaacgcgtccgggcctgtcccgccctctccccaagcgcgqqcccqqccaqc 61 ggaagcccctgcgcccgcgccatgtcaaagaaaaaggactgagtgcagaagaaaagaga 121 actcgcatgatggaaatattttctgaaacaaaagatgtatttcaattaaaagacttggag 181 aagattgctcccaaagagaaaggcattactgctatgtcagtaaaagaagtccttcaaagc 241 ttagttgatgatggtatggttgactgtgagaggatcggaacttctaattattattgqqct 301 tttccaagtaaagctcttcatgcaaggaaacataagttggaggttctggaatctcaggac 361 cctggctgcttccatgaaataattaaagtctcctattatagaaaattctgqctqqqc 421 gcagtggctcacgcctgtaatcccagcactttgggaggctgaggcgggcagatcacgagg 1 M K C K M E L S E G S O K H 481 tgactttccccacccccacATGAAGTGCAAGATGGAGTTGTCTGAGGGAAGTCAAAAGC 15 SLQKSIEKAKIGRCET 541 ATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGC R L A K E L S S L R D O R E O L K A E 601 GAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAG EKYKDCDPQVVEEIROANK 661 AAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATA V A K E A A N R W T D N I F A I K S W A 721 AAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGG 95 FGFEENKIDRTFGI 781 CCAAAAGAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGGAATTCCAGAAG 115 F D Y I D \* 841 ACTTTGACTACATAGACTAAaatattccatggtggtgaaggatgtacaagcttgtgaata 901 tgtaaattttaaactattatctaactaagtgtactgaattgtcgttttgcctgtaactgtg 1021 aaaaaaaa

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 4 of 36

Figure 2D. The cDNA (SEQ ID. NO:8) and amino acid sequence (SEQ ID. NO:9) of 121P1F1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.



Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN
ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 5 of 3

Figure 2E. The cDNA (SEQ ID. NO:10) and amino acid sequence (SEQ ID. NO:11) of 121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid 82-654 including the stop codon.

1	cc	aaa.	atc	aaa	cgc	gtc	cgg	gcc	tgt	ccc	gee	cct	ctc	ccc	aag	cgc	ggg	ccc	ggc	cagc
1								M	s	K	K	K	G	L	S	Α	E	Ė	K	R
61	gg	aag	ccc	ctg	cgc	ccg	cgc	cAT	<u>G</u> TC	AAA	GAA	AAA	AGG	ACT	GAG'	TGC	AGA	AGA	AAA	GAGA
14	T	R	М	М	E	I	F	S	E	$\mathbf{T}$	K	D	V	F	Q	L	K	D	L	E
121	AC	TCG	CAT	GAT	GGA.	AAT	TTA	TTC	TGA	AAC.	AAA	AGA'	TGT	ATT'	гсал	ATTA	AAA	AGA	CTT	GGAG
34	K	I	А	Р	K	E.	K	G	I	T	А	M	S	V	K	E	V	L	Q	S
181	AΆ	GAT'	TGC'	TCC	CAA	AGA	GAA	AGG	CAT	rac'	rgc'	ГАТ	GTC	AGT	AAA	AGA	AGT	CCT'	гсал	AAGC
54	L	V	D	D	G	М	V	D	С	E	R	I	G	T	S	N	Y	Y	W	А
241	ТТ	AGT'	TGA'	TGA:	rgg'	TAT	GGT	TGA	CTG'	rga(	GAG	GAT	CGG	AAC'	rrc'	raa'	TTA	rta'	rtg	GGCT
74	F	P	S	K	Α	L	Н	А	R	K	Н	K	$_{ m L}$	E	V	L	E	S	Q	L
301	тт	TCC	AAG'	TAA	AGC'	rct'	ГСА	TGC.	AAG	GAA	ACA	ΓAΑ	GTT	GGA(	GGT	rcto	GGA <i>i</i>	ATC	rca(	STTG
94	S	E	G	S	Q	K	Н	Α	S	L	Q	K	S	I	Ė	K	A	K	I	G
361	TC	TGA	GGG	AAG	rca.	AAA	GCA	TGC	AAG	CCT	ACA	GAA	AAG	CAT	rga(	GAA	AGC	raa <i>i</i>	AAT	rggc
114	R	С	E	T	E	E	R	Т	R	L	A	K	E	L	S	S	L .	R	D	Q
421	CG	ATG	rga/	AAC	GGA/	AGA	GCG.	AAC	CAG	GCT	AGC/	AAA	AGA	GCT:	rrc	гтса	ACT	rcg	AGA	CCAA
134	R	E	Q	L	K	A	E	V	E	K	Y	K	D	С	D	Р	Q	V	V	E
481	AG	GGA/	ACA(	GCTA	AAA	GGC	AGA.	AGT	AGA/	\AA;	ATA	CAA	AGA	CTG	rga:	rcc	GCA	AGT:	rgro	GGAA
154	E	I	Н	N	I	F	A	I	K	S	M	А	K	R	K	F	G	F	E	E
541	GA	AATA	ACA!	raa(	CAT	TTA	CGC.	AAT	AAAA	ATC	ГТG	GGC	CAA	AAGA	AAA	TTF	rgg	GTT:	rga <i>i</i>	AGAA
174	N	K	I	D	R	$\mathbf{T}$	F	G	Ι	P	E	D	F	D	Y	I	D	*		
601	AA	TAA	TAP	rga:	raga	AAC:	rtt'	TGG	TAP	rcci	AGA/	AGA(	CTT	rgad	CTAC	CATA	AGA(	CTA	\aat	att
661	CC	atg	gtg	gtga	aag	gato	gta	caa	gctt	gt	gaat	ato	gtaa	aatt	itta	aaa	ctat	tat	cta	act
721	aa	gtgt	tact	tgaa	att	gtc	gtt	tgc	ctgt	aad	ctgt	gti	ttat	cat	ttt	att	caat	gtt	aaa	ataa
781	ag	tgta	aaaa	atgo	caaa	aaaa	aaa	aaaa	aaaa	aaaa	aaaa	aaa	aaaa	aaaa	a					

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 6 of 36

Figure 2F. The cDNA (SEQ ID. NO:12) and amino acid sequence (SEQ ID. NO:13) of 121P1F1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid 281-853 including the stop codon.

1 gttttctgtattgtaatatgtagagcacattccagaactgctcagtttcgagttacctaa 61 tggatcttcactgtgtgccaattagtcgatttctgtgaaaacgccccggtttctgccaaa 121 gggcaggagtcgctgctcttgtgccgggtgctgctggttgtgtagggcqctqttqctttt 181 ttaaggacgetetgeactgaattaggetteetegtgggteatgateagttaagteetqte 1 MMEIFSE 241 aaagaaaaaggactgagtgcagaagaaaagagaactcgcATGATGGAAATATTTTCTGA K D V F Q L K D L E K I A P K E K G 301 AACAAAAGATGTATTTCAATTAAAAGACTTGGAGAAGATTGCTCCCAAAGAGAAAGGCAT A M S V K E V L Q S L V D D G M V D C 361 TACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGCTTAGTTGATGATGGTATGGTTGACTG R T G T S N Y Y W A F P S K A L H 421 TGAGAGGATCGGAACTTCTAATTATTGGGCTTTTCCAAGTAAAGCTCTTCATGCAAG K H K L E V L E S O L S E G S O K H A S 481 GAAACATAAGTTGGAGGTTCTGGAATCTCAGTTGTCTGAGGGAAGTCAAAAGCATGCAAG LQKSIEKAKIGRCETEERT 541 CCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGCGAACCAG LAKELSSLRDQREQLKAEVE 601 GCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAGAAGTAGA 128 KYKDCDPQVVEEI RQANKVA 661 AAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATAAAGTAGC EAANRWTDNIFAIKSWA 148 721 CAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGGCCAAAAG FGFEENKIDRTFG 781 AAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGGAATTCCAGAAGACTTTGA 188 I D 841 CTACATAGACTAAaatattccatggtggtgaaggatgtacaagcttgtgaatatgtaaat 901 tttaaactattatctaactaagtgtactgaattgtcgttttgcctgtaactgtgtttatca 961 ttttattaatgttaaataaagtgtaaaatgcagatgttcttcaccccttttggtagaaca 1021 aaagcaggatgataaccatatccccccagtgctcatcaaagtaggacactaaaaatccat 1081 ccatctcagtcaaagtcgagcggccgcgaatttagtagtagtagcggccgctctagagga  $1141 \ {\tt tccaagcttacgtacgcgtgcatgcgacgtcatagctcttctatagtgtcacctaaattc}$ 1201 aagtt

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN
ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 7 of 36

Figure 3:

Figure 3A. Amino acid sequence of 121P1F1 (SEQ ID. NO:14). The 121P1F1 protein has 205 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LOSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
- 121 TRLAKELSSL RDOREQLKAE VEKYKDCDPO VVEEIROANK VAKEAANRWT DNIFAIKSWA
- 181 KRKFGFEENK IDRTFGIPED FDYID

Figure 3B. Amino acid sequence of 121P1F1 splice variant 1A (SEQ ID. NO:15). The 121P1F1 splice variant 1A protein has 126 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQDPGCCFHE IIKVSYYRKF WLGAVAHACN
- 121 PSTLGG

Figure 3C. Amino acid sequence of 121P1F1 splice variant 1B (SEQ ID. NO:16). The 121P1F1 splice variant 1B protein has 119 amino acids.

- 1 MKCKMELSEG SQKHASLQKS IEKAKIGRCE TEERTRLAKE LSSLRDQREQ LKAEVEKYKD
- 61 CDPQVVEEIR QANKVAKEAA NRWTDNIFAI KSWAKRKFGF EENKIDRTFG IPEDFDYID

Figure 3D. Amino acid sequence of 121P1F1 splice variant 2 (SEQ ID. NO:17). The 121P1F1 splice variant 2 protein has 122 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETAKO
- 121 IK

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 8 of 36

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO:18). The 121P1F1 splice variant 3 protein has 190 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
- 121 TRLAKELSSL RDQREQLKAE VEKYKDCDPQ VVEEIHNIFA IKSWAKRKFG FEENKIDRTF
- 181 GIPEDFDYID

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO:19). The 121P1F1 splice variant 4 protein has 190 amino acids.

- 1 MMEIFSETKD VFQLKDLEKI APKEKGITAM SVKEVLQSLV DDGMVDCERI GTSNYYWAFP
- 61 SKALHARKHK LEVLESQLSE GSQKHASLQK SIEKAKIGRC ETEERTRLAK ELSSLRDQRE
- 121 QLKAEVEKYK DCDPQVVEEI RQANKVAKEA ANRWTDNIFA IKSWAKRKFG FEENKIDRTF
- 181 GIPEDFDYID

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 9 of 36

#### Figure 4A

#### Amino Acid Alignments.

Alignment of 121P1F1 protein and its variants.

#### A) CLUSTAL W alignment of 121P1F1 and variants 1-3. (SEQ ID NOS: 3, 5, 7, 9 and 11)

121P1F01 sv1A sv1B sv-2 sv-3	MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEMSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEMKCKMELSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQREMSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEMSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKE
121P1F01 sv1A sv1B sv-2 sv-3	VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK-HASLQKS-I VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQDP-GCCF-HEIIKVSYY QLKAEVEK-YKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKID VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK-HASLQKS-I VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK-HASLQKS-I
121P1F01 sv1A sv1B sv-2 sv-3	EKAKIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAAN RKFWLGAVAHACNPSTLGG
121P1F01 sv1A sv1B sv-2 sv-3	RWTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDFDYID

#### Figure 4B

#### B) Clustal alignment of 121P1F1 and variants 1A and 4 (SEQ ID NOS 3, 13 and 5)

2	sv-4	MSKKKGLSAEEKRTR	16 30 MMEIFSETKDVFQLK MMEIFSETKDVFQLK MMEIFSETKDVFQLK	DLEKIAPKEKGITAM DLEKIAPKEKGITAM	SVKEVLQSLVDDGMV	DCERIGTSNYYWAFP DCERIGTSNYYWAFP	SKALHARKHKLEVLE
2	121P1F01 sv-4 sv-1A	SQLSEGSQKHASLQK SQLSEGSQKHASLQK	106 120 SIEKAKIGRCETEER SIEKAKIGRCETEER YYRKFWLG	TRLAKELSSLRDQRE TRLAKELSSLRDQRE	QLKAEVEKYKDCDPQ QLKAEVEKYKDCDPQ	VVEEIRQANKVAKEA VVEEIRQANKVAKEA	ANRWTDNIFAIKSWA
2	121P1F01 sv-4 sv-1A	181 195 KRKFGFEENKIDRTF KRKFGFEENKIDRTF	GIPEDFDYID 190	211			

App No.: 10/087,190 Inventor: Pia M. CHALLITA-EID et al. Docket No.: 511582003420

Sbjct: 181 KRKFGFEENKIDRTFGIPEDFDYID 205

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 10 of 36

#### Figure 4C

# C) Alignment of 121P1F1 and variant 1 (SEQ ID NO:20) with human GAJ (SEQ ID NO:21) Identities = 205/205 (100%), Positives = 205/205 (100%)

121P	1:	1	${\tt MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV}$	60
			MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV	
Sbjc	t:	1	${\tt MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV}$	60
121P	1:	61	DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER	120
			DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLOKSIEKAKIGRCETEER	
Sbjc	t :	61	DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER	120
0~)0	٠.	0.1	PODMICTOR TOTAL DIMENSION DE LA PROPERTIE DE L	120
1210	1.	1 2 1	THE AVEL COLD DODGOL VA PURIVAVDOD DOLLARDA DOLLARDA DOLLARDA DALARDA	100
1215	т:	121	${\tt TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA}$	180
			TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA	
Sbjc	t:	121	TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA	180
~				100
121P	1.	181	KRKFGFEENKIDRTFGIPEDFDYID 205	
*~ **	٠.	101		
			KRKFGFEENKIDRTFGIPEDFDYID	

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 11 of 36

#### Figure 4D

#### D) Alignment of 121P1F1 and variant 1 (SEQ ID NO:22) with closest mouse homolog, a hypothetical 24.2 KDa protein. (SEQ ID NO:23)

Identities = 183/205 (89%), Positives = 193/205 (93%)

121P1: 1	MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
	MSKK+GLS EEKRTRMMEIF ETKDVFQLKDLEK+APKEKGITAMSVKEVLQSLVDDGMV
Chiot. 1	MCVVDCI CCPRVDEDAMOT DEDEMONEOT VOLENT A DIRECTEDAMON DE CONTRA C

Sbjct: 1 MSKKRGLSGEEKRTRMMEIFFETKDVFQLKDLEKLAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120 DCERIGTSNYYWAFPSKALHARK KLE L SQLSEGSQKHA LQKSIEKA++GR ETEER

Sbjct: 61 DCERIGTSNYYWAFPSKALHARKRKLEALNSQLSEGSQKHADLQKSIEKARVGRQETEER 120

121P1: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180 LAKEL S RDQR+QLKAEVEKY++CDPQVVEEIR+ANKVAKEAANRWTDNIFAIKSWA

Sbjct: 121 AMLAKELFSFRDQRQQLKAEVEKYRECDPQVVEEIREANKVAKEAANRWTDNIFAIKSWA 180

121P1: 181 KRKFGFEENKIDRTFGIPEDFDYID 205

KRKFGFEE+KID+ FGIPEDFDYID

Sbjct: 181 KRKFGFEESKIDKNFGIPEDFDYID 205

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#### Figure 4E

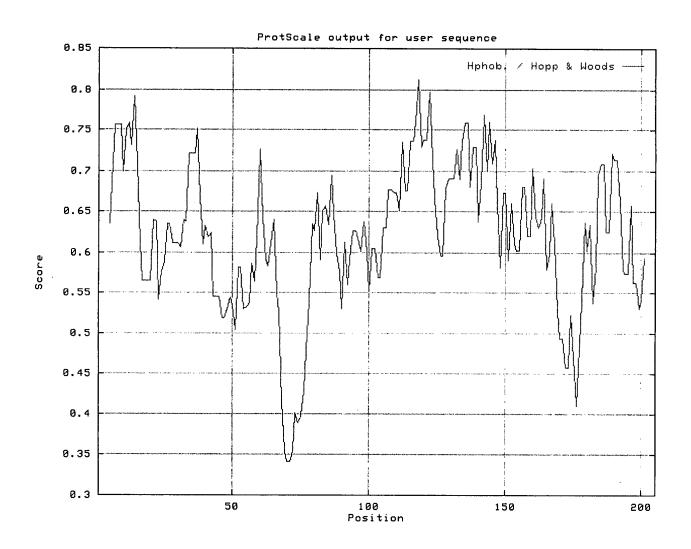
E) Alignment of 121P1F1 and variant 1 (SEQ ID NO:24) with>gi|1175412|sp|Q09739|YA53 SCHPO HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I (SEQ ID NO:25) gi|7490680|pir||T37610 hypothetical coiled-coil protein fission yeast (Schizosaccharomyces pombe) gi|984224|emb|CAA90804.1| (Z54096) hypothetical coiled-coil protein [Schizosaccharomyces pombe] Length = 210Score = 121 bits (305), Expect = 5e-27Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps = 6/202 (2%) Query: 5 KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64 KGLS EKR R+ IF ++KD FQLK++EK+ KKI +VK+VLOSLVDD +V E+KGLSLAEKRRRLEAIFHDSKDFFQLKEVEKLGSK-KOIVLOTVKDVLOSLVDDNIVKTEK 62 Query: 65 IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGR----CETEER 120 IGTSNYYW+FPS A +R+ L L++QL + QK +L ++IK R E + Sbict: 63 IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN 122 Query: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180 + L + + + LK ++ C+P+ E + K EAAN WTD I + ++ Sbjct: 123 QYTLELLHAKESELKLLKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC 182 Query: 181 KRKFGFEENKIDRTFGIPEDFD 202 G + N+IIPED D Sbjct: 183 -RDMGADTNQIREYCSIPEDLD 203

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Title: NUCLEIC ACID AND CORRESPONDING PROTEIN
ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 13 of 36

# Figure 5A 121P1F1 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

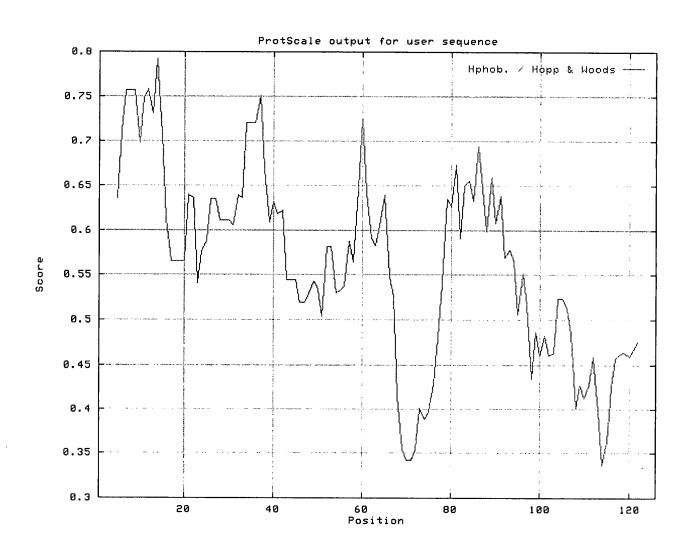


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ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 14 of 36

# Figure 5B 121P1F1 variant 1a Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

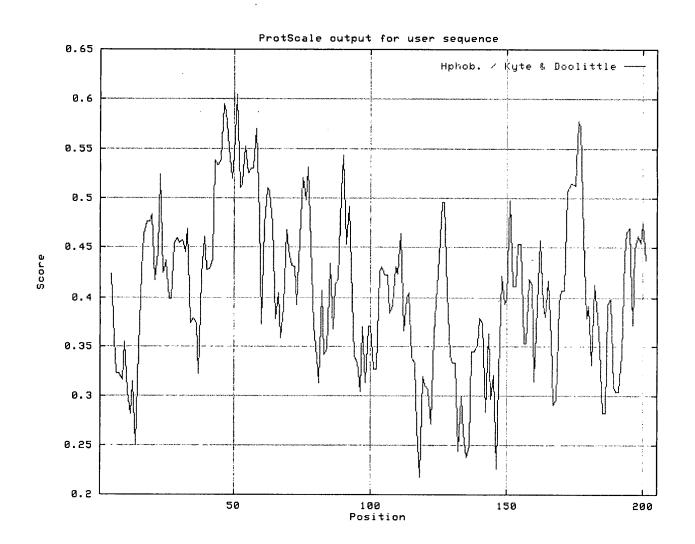


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ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET Sheet 15 of 36

# Figure 6A 121P1F1 Hydropathicity Profile

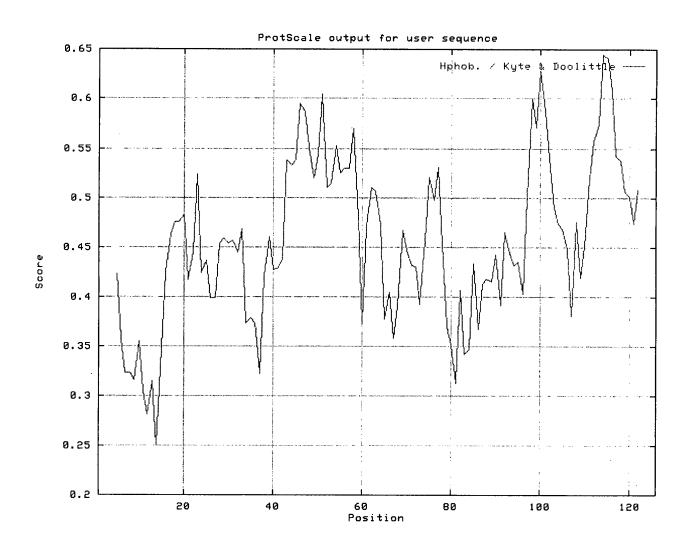
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)



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ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 16 of 36

### Figure 6B 121P1F1 variant 1a Hydropathicity Profile (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

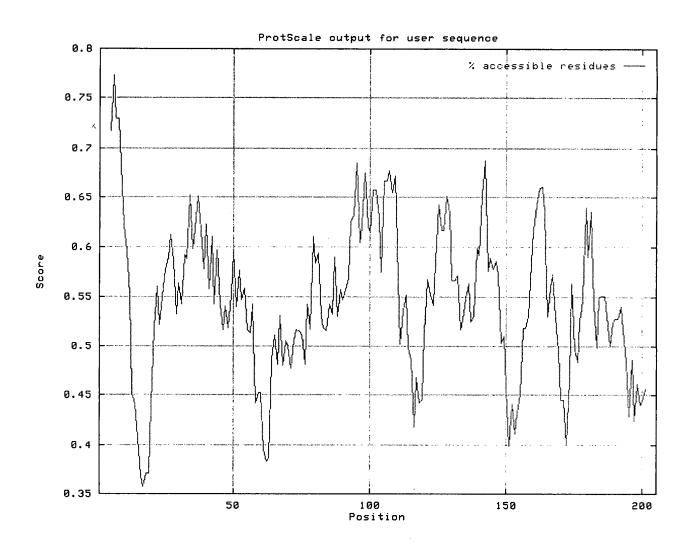


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# Figure 7A 121P1F1 % Accessible Residues Profile

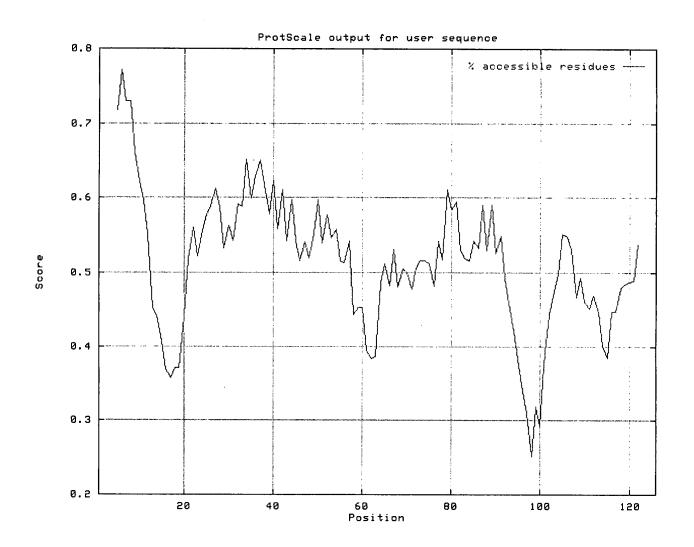
(Janin J., 1979. Nature 277:491-492)



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Figure 7B
121P1F1 variant 1a % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

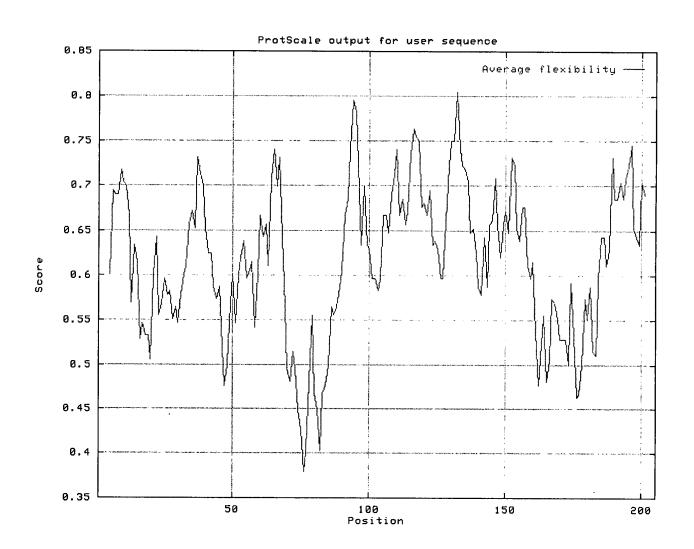


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# Figure 8A 121P1F1 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

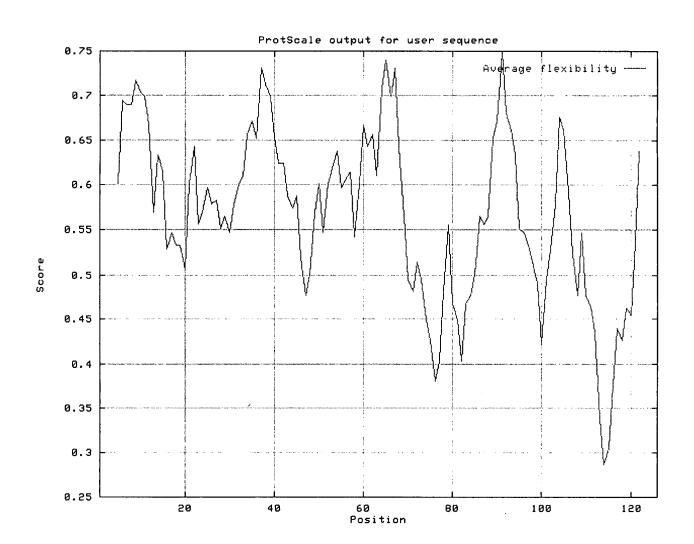


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ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 20 of 36

# Figure 8B 121P1F1 variant 1a Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

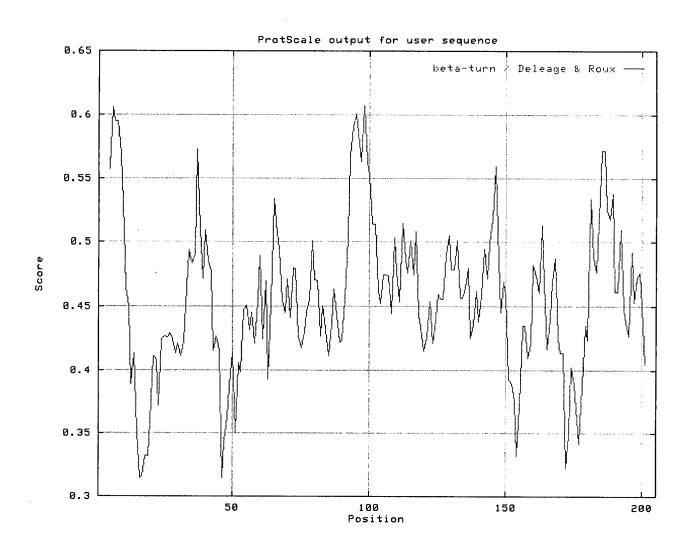


Inventor: Pia M. CHALLITA-EID et al.

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ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 21 of 36

## Figure 9A 121P1F1 Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

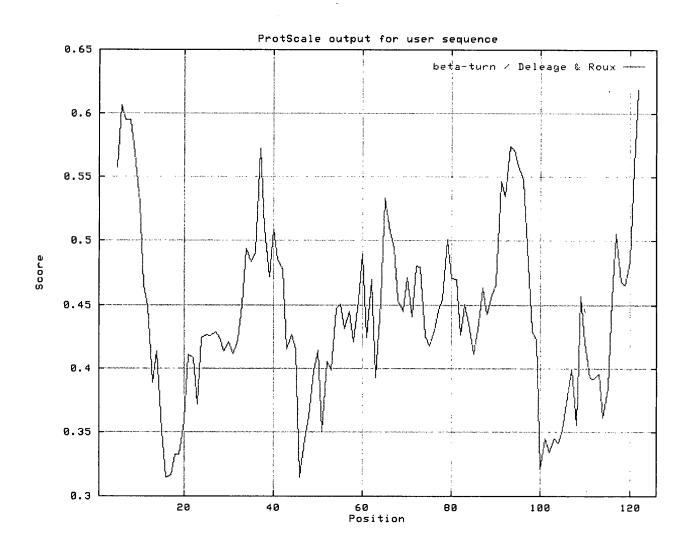


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# Figure 9B 121P1F1 variant 1a Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



REPLACEMENT SHEET Figure 10 1 1) 867 121P1F01 867 bp 358 518 1(1) 1028(867) 2) 121P1F01 v.1 1028 bp 1(1) 432(432) 433(548) 752(867) 3) 121P1F01 v.2 752 bp 4) 1(1) 822(867) 547(547)548(593) 1 21P1F01 v.3 822 bp 5) 239(85) 992(838) 1 21P1F01 v.4 1025 bp 993 1205 238 1

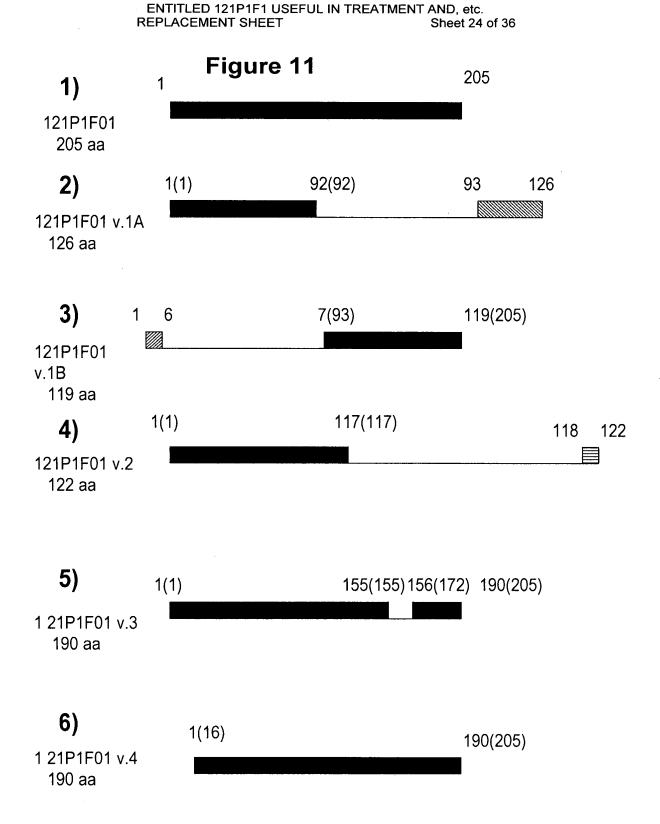
Docket No.: 511582003420

App No.: 10/087,190

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.

Note: Numbers in "()" correspond to those of the original sequence. Black box shows the same sequence as the original one. SNPs are indicated above the box.



Docket No.: 511582003420

App No.: 10/087,190

Inventor: Pia M. CHALLITA-EID et al.

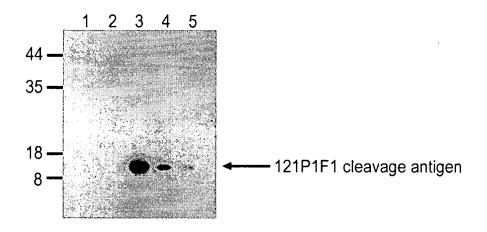
Title: NUCLEIC ACID AND CORRESPONDING PROTEIN

Note: Numbers in "()" correspond to those of the original sequence. Black box shows the same sequence as the original one. Single amino acid variations are indicated above the box.

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 25 of 36

Figure 12
Specific recognition of 121P1F1 antigen by anti-121P1F1 pAb



1.	Pre-immune	1:100
2.	Pre-immune	1:1,600
3.	Anti-121P1F1 serum	1:100
4.	Anti-121P1F1 serum	1:400
5	Anti-121P1F1 serum	1.1 600

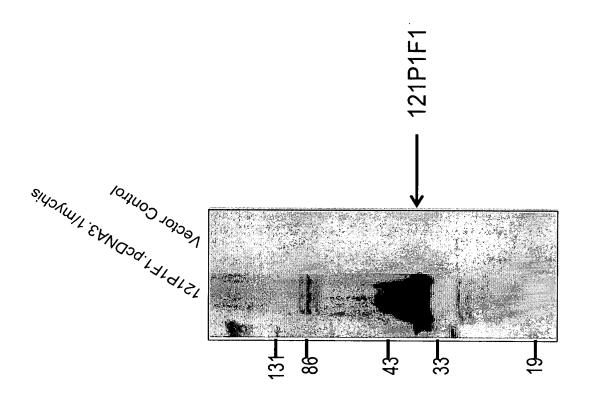
App No.: 10/087,190 Docket No.: 511582003420 Inventor: Pia M. CHALLITA-EID et al. Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. (E) Silealoled SANA SANA (E) SILEA ( REPLACEMENT SHEET Sheet 26 of 36 (E) 40/03/0107 Figure 13 Expression of 121P1F1 in various cancer cells (8) 40/0s) 2.0083 (E) OUNI) ZOHIJAN (E) 1000 (E) 100 (E) 1 (6) OUOD) ST. CH (6) 01/09/SOH (8) 8/100) SO 27 (S/180 ABUDIN S/UDAGE) LEGE LATATES WINDS AND LEGE 36-22 <del>6</del>

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.

REPLACEMENT SHEET

Sheet 27 of 36



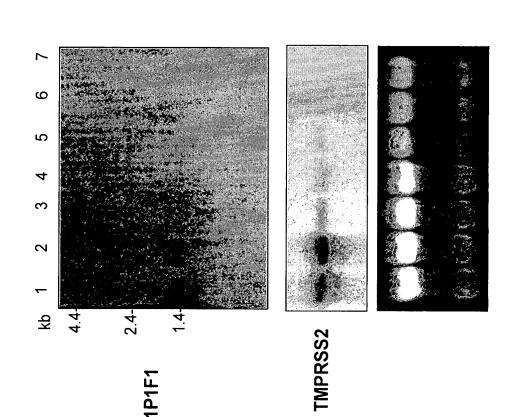
Inventor: Pia M. CHALLITA-EID et al.

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REPLACEMENT SHEET

Figure 15 121P1F1 Androgen Regulation In Vivo

LAPC-9AD Day 0 LAPC-9AD Day 0 LAPC-9AD Day 7 LAPC-9AD Day 7 LAPC-9AD Day 15 LAPC-9AD Day 15 LAPC-9AD Day 15 - 7 6 7 4 4 6 6 K



Docket No.: 511582003420

App No.: 10/087,190 Docket No.: 51158200 Inventor: Pia M. CHALLITA-EID et al.
Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.

REPLACEMENT SHEET

Sheet 29 of 36

Figure ToA Secondary structure prediction of 121P1F		121P1F
Figure 10A Secondary structure prediction		of
rigure Secondary structure	HOI	prediction
Secondary	rigure	structure
		Secondary

	10	20	30	40	50	09	70
		_					_
MSKKKGL	SAEEKRTRMME	EIFSETKDVFÇ	OLKDLEKIAPI	KEKGITAMSVF	KEVLQSLVDDK	MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNY	NY
) ) ) ) ) ) )	շհհհհհհհհհհ	հհհհետերհե	ռհհհհհհհե	сссррррр	ւհհհհհհհհե	ссссссстринтинтинтинтинтинтинтинтинтинтесссствитинтинтинтинтесссств	Ŋ
YWAFPSK	ALHARKHKLEN	VLESQLSEGSÇ	) KHASLQKSII	SKAKIGRCETE	ERTRLAKEL!	YWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQREQLKAE	AE
eeeccch	eeeccchhhhhhhccehh	hhhhccccc	կրրրիրիրի Մարդերիրի	հեհեշշշեր	ւհեհեհեհերհ	ећћћћћ тос с с с с с б та прави	hh
VEKYKDCI	DPQVVEEIRQ <i>i</i>	VEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDFDYID	KWTDNIFAIKS	SWAKRKFGFEE	NKIDRTFGI	PEDFDYID	
hhhhccc	сссррррррр	ининсесссснинининининининининининининини	կերհերհերհ <u>ի</u>	հերհեր	וכככככככככ	מממממממ	

Alpha helix (h): 61.95% Extended strand (e): 1.95% Random coil (c): 36.10%

App No.: 10/087,190 Inventor: Pia M. CHALLITA-EID et al. Docket No.: 511582003420

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.

REPLACEMENT SHEET

Sheet 30 of 36

Figure 16B

# Secondary structure prediction of variant 1a

10	50	30	40	20	09	70
		_		_	_	_
KGLSAEEK.	RTRMMEIFSETK	MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNY	APKEKGITAN	MSVKEVLQSLV	/DDGMVDCER]	GTSNY
ccchhhh	հհհհհհհհհե	ссссссструнти при при при при при при при при прессссо при при при при при прессссо пресссо пресссо пресссо пре	ccccchhh	դդդդդդդդդդ	hccccchhcc	22222
SKALHAR	KHKLEVLESQDE	YWAFPSKALHARKHKLEVLESQDPGCCFHEIIKVSYYRKFWLGAVAHACNPSTLGG	YYRKFWLGA	VAHACNPSTLG	5,	
chhhhh	cceeeeeccc	eeeccchhhhhcccceeeeeccccchhhhhhhhhhhhcceecccccc	hhhhhhhcce	ooooooooe	ς,	

Alpha helix (h): 50.79% Extended strand (e): 7.94% Random coil (c): 41.27%

App No.: 10/087,190

Docket No.: 511582003420

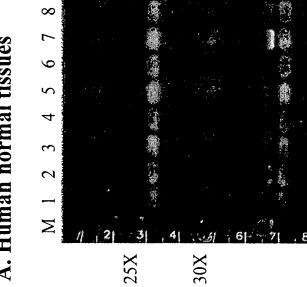
Inventor: Pia M. CHALLITA-EID et al

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REPLACEMENT SHEET

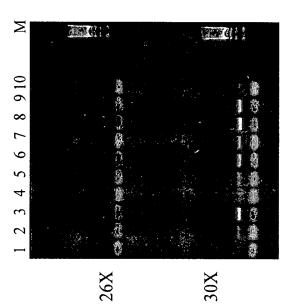
Sheet 31 of 36

A. Human normal tissues



B. Patient tumor specimens

Figure 17 Expression of 121P1F1 by RT-PCR



1) VP1

5) Small Int.

1) Colon

6) Spleen

2) Ovary

7) Testis

3) Leuk.

- 6) Bladder cancer pool
- 7) Kidney cancer pool

2) VP2

3) XP

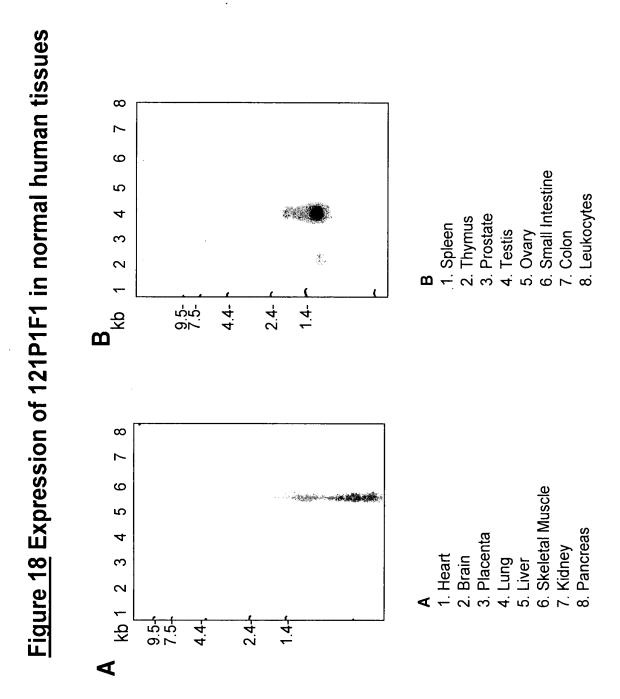
- 8) Colon cancer pool
  - 9) Lung tumor
  - 4) Normal prostate

8) Thymus

4) Prost.

- 5) Prostate cancer pool 10) H2O

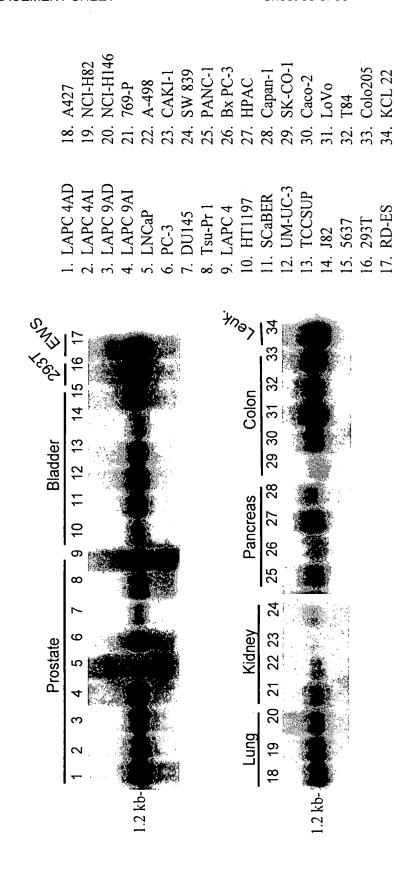
App No.: 10/087,190 Docket No.: 511582003420 Inventor: Pia M. CHALLITA-EID et al.
Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET Sheet 32 of 36



App No.: 10/087,190 Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN
ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
Sheet 33 of 36

Figure 19 Expression of 121P1F1 in Multiple Cancer Cell lines



Docket No.: 511582003420

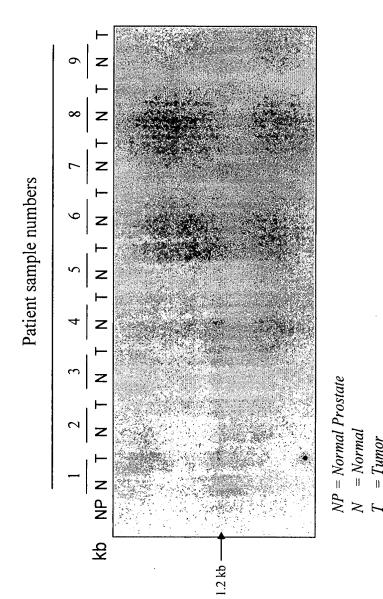
App No.: 10/087,190 Docket No.: 51158200 Inventor: Pia M. CHALLITA-EID et al.
Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.

REPLACEMENT SHEET

Figure 20 Expression of 121P1F1 in Patient Prostate Cancer Samples

Sheet 34 of 36

= Tumor



Docket No.: 511582003420

App No.: 10/087,190 Docket No.: 51158200
Inventor: Pia M. CHALLITA-EID et al.
Title: NUCLEIC ACID AND CORRESPONDING PROTEIN
ENTITLED 1219171 USEFUL IN TREATMENT AND, etc.

REPLACEMENT SHEET

Sheet 35 of 36

# Figure 21 Expression of 121P1F1 in Kidney, Breast, Cervical and Stomach Patients Samples as well as Cancer Cell lines

kidne Z

breast



N = normal adjacent tissue RNA

T = tumor RNA

cervix

stomach

Cancer cell lines are: (from left to right)

Daudi (Burkitt's lymphoma) HeLa (cervical carcinoma) K562 (CML)

HL-60 (PML)

MOLT-4 (lymphoblastic leuk.) A549 (lung carcinoma) G361 (melanoma)

SW480 (colorectal carcinoma) Raji (Burkitt's lymphoma)

Cell Lines

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1. LAPC-42 FBS

REPLACEMENT SHEET

**Sheet 36 of 36** 

Figure 22 Androgen Regulation of 121P1F1

